



PCT10

## RAW SEQUENCE LISTING

DATE: 02/21/2003

PATENT APPLICATION: US/10/009,916A

TIME: 10:08:21

Input Set : N:\CrF4\01212003\J009916.raw

Output Set: N:\CRF4\02212003\J009916A.raw

1 <110> APPLICANT: Ankenbauer, Robert G.  
 2 Hasse, Detlef  
 3 Panaccio, Michael  
 4 Rosey, Everett Lee  
 5 Wright, Catherine  
 6 <120> TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED SODC  
 7 POLYPEPTIDES, PEPTIDES, AND PROTEINS AND THEIR USES  
 8 <130> FILE REFERENCE: DAVI148.001APC  
 9 <140> CURRENT APPLICATION NUMBER: US/10/009,916A  
 10 <141> CURRENT FILING DATE: 2001-11-13  
 11 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00436  
 12 <151> PRIOR FILING DATE: 2000-05-11  
 13 <150> PRIOR APPLICATION NUMBER: US 60/133,989  
 14 <151> PRIOR FILING DATE: 1999-05-13  
 15 <160> NUMBER OF SEQ ID NOS: 13  
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 180  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: Lawsonia intracellularis  
 22 <400> SEQUENCE: 1  
 23 Met Lys Ile Lys Leu Phe Phe Val Thr Ser Ile Val Thr Ile Ser Leu  
 24 1 5 10 15  
 25 Leu Thr Ser Ile Thr Ser Val Val Leu Ala Cys Ser Val Thr Ser Glu  
 26 20 25 30  
 27 Val His Met Ile Asp Asp Asn Gly Ile Lys Gln Ser Ile Gly Thr Val  
 28 35 40 45  
 29 Thr Phe Thr Asp Thr Asp Lys Gly Leu Gln Ile Lys Thr Asp Leu Lys  
 30 50 55 60  
 31 Gly Leu Pro Ala Gly Glu His Gly Phe His Ile His Glu Gly Gly Ser  
 32 65 70 75 80  
 33 Cys Gly Pro Ala Glu His Asp Gly His Leu Thr Ala Gly Leu Gln Ala  
 34 85 90 95  
 35 His Gly His Tyr Asp Pro Asp Lys Thr Gly Lys His Glu Gly Pro Leu  
 36 100 105 110  
 37 Gly Asn Gly His Lys Gly Asp Leu Pro Arg Leu Val Val Lys Ala Asp  
 38 115 120 125  
 39 Gly Ile Ala Lys Glu Thr Leu Leu Ala Pro Arg Leu Thr Val Lys Glu  
 40 130 135 140  
 41 Ile Lys Gly Arg Thr Val Met Ile His Ala Gly Gly Asp Asn Tyr Ser  
 42 145 150 155 160  
 43 Asp Lys Pro Leu Pro Leu Gly Gly Gly Gly Ala Arg Ile Ala Cys Gly  
 44 165 170 175

ENTERED

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```

45      Val Ile Pro Asn
46                      180
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 543
50 <212> TYPE: DNA
51 <213> ORGANISM: Lawsonia intracellularis
52 <220> FEATURE:
53 <221> NAME/KEY: CDS
54 <222> LOCATION: (1)...(543)
55 <400> SEQUENCE: 2
56      atg aaa ata aaa cta ttt ttt gtt act tca ata gta act att tct ctc      48
57      Met Lys Ile Lys Leu Phe Phe Val Thr Ser Ile Val Thr Ile Ser Leu
58          1                      5                      10                      15
59      tta act agt att act agt gta gta tta gca tgt tct gtt act tca gaa      96
60      Leu Thr Ser Ile Thr Ser Val Val Leu Ala Cys Ser Val Thr Ser Glu
61          20                      25                      30
62      gtc cat atg att gat gac aat gga ata aaa cag agt ata ggc aca gta      144
63      Val His Met Ile Asp Asp Asn Gly Ile Lys Gln Ser Ile Gly Thr Val
64          35                      40                      45
65      act ttt act gat aca gat aaa ggt cta caa ata aaa act gat ctt aaa      192
66      Thr Phe Thr Asp Thr Asp Lys Gly Leu Gln Ile Lys Thr Asp Leu Lys
67          50                      55                      60
68      ggc ctt cct gca gga gaa cat ggt ttt cat atc cat gaa gga gga tca      240
69      Gly Leu Pro Ala Gly Glu His Gly Phe His Ile His Glu Gly Gly Ser
70          65                      70                      75                      80
71      tgt gga cct gct gag cat gat gga cat cta aca gct gga ctc caa gct      288
72      Cys Gly Pro Ala Glu His Asp Gly His Leu Thr Ala Gly Leu Gln Ala
73          85                      90                      95
74      cat ggt cat tat gat cct gac aaa aca gga aaa cat gaa gga cct ctt      336
75      His Gly His Tyr Asp Pro Asp Lys Thr Gly Lys His Glu Gly Pro Leu
76          100                     105                     110
77      ggt aat gga cac aag gga gac tta cct aga ctt gta gtt aaa gct gat      384
78      Gly Asn Gly His Lys Gly Asp Leu Pro Arg Leu Val Val Lys Ala Asp
79          115                     120                     125
80      gga ata gca aaa gaa aca ctc tta gct cca aga tta aca gtt aaa gaa      432
81      Gly Ile Ala Lys Glu Thr Leu Leu Ala Pro Arg Leu Thr Val Lys Glu
82          130                     135                     140
83      att aag ggt cgt aca gtt atg atc cat gct ggt ggt gat aac tat tca      480
84      Ile Lys Gly Arg Thr Val Met Ile His Ala Gly Gly Asp Asn Tyr Ser
85          145                     150                     155                     160
86      gat aaa cct ctt cct ctt ggc ggt ggt ggt gct cgt ata gct tgt ggt      528
87      Asp Lys Pro Leu Pro Leu Gly Gly Gly Gly Ala Arg Ile Ala Cys Gly
88          165                     170                     175
89      gtt ata cca aac tag      543
90      Val Ile Pro Asn *
91          180
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 10
95 <212> TYPE: PRT

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96 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Protective peptide leader sequence.
99 <400> SEQUENCE: 3
100      . Met Gly Thr Thr Thr Thr Thr Ser Leu
101      1              5              10
103 <210> SEQ ID NO: 4
104 <211> LENGTH: 58
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Forward Primer RA167.
109 <400> SEQUENCE: 4
110      ggccatgggt accaccacca ccaccacctc tctgtctgtt acttcagaag tccatatg      58
112 <210> SEQ ID NO: 5
113 <211> LENGTH: 33
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Reverse Primer RA175.
118 <400> SEQUENCE: 5
119      ggctctagag gtatataaat ataaagaggt atg      33
121 <210> SEQ ID NO: 6
122 <211> LENGTH: 42
123 <212> TYPE: PRT
124 <213> ORGANISM: Lawsonia intracellularis
125 <400> SEQUENCE: 6
126      Met Lys Ile Lys Leu Phe Phe Val Thr Ser Ile Val Thr Ile Ser Leu
127      1              5              10              15
128      Leu Thr Ser Ile Thr Ser Val Val Leu Ala Cys Ser Val Thr Ser Glu
129      20              25              30
130      Val His Met Ile Asp Asp Asn Gly Ile Lys
131      35              40
133 <210> SEQ ID NO: 7
134 <211> LENGTH: 172
135 <212> TYPE: PRT
136 <213> ORGANISM: Escherichia coli
137 <400> SEQUENCE: 7
138      Met Lys Arg Phe Ser Leu Ala Ile Leu Ala Val Val Ala Thr Gly Ala
139      1              5              10              15
140      Ala Ser Glu Lys Gln Ala Val Glu Met Asn Leu Val Thr Ser Gln Gly
141      20              25              30
142      Val Gly Gln Ser Ile Gly Ser Val Thr Ile Thr Glu Thr Asp Lys Gly
143      35              40              45
144      Leu Glu Phe Ser Pro Asp Leu Lys Ala Leu Pro Pro Gly Glu His Gly
145      50              55              60
146      Phe His Ile His Ala Lys Gly Ser Cys Gln Pro Ala Thr Lys Asn Trp
147      65              70              75              80
148      Asp Gly Lys Ala Thr Asp Ala Val Ile Ala Pro Arg Leu Lys Asp Gly

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149          85          90          95
150      Lys Ala Ser Ala Ala Glu Ser Ala Gly Gly His Leu Asp Pro Gln Trp
151          100          105          110
152      Thr Gly Ser Leu Asp Glu Ile Lys Asp Lys Ala Leu Met Val His Val
153          115          120          125
154      Gly Gly Asp Asn Met Ser Lys His Glu Gly Pro Glu Gly Ala Gly His
155          130          135          140
156      Leu Gly Asp Leu Pro Ala Leu Val Val Asp Gln Pro Lys Pro Leu Gly
157      145          150          155          160
158      Gly Gly Gly Glu Arg Tyr Ala Cys Gly Val Ile Lys
159          165          170
161 <210> SEQ ID NO: 8
162 <211> LENGTH: 177
163 <212> TYPE: PRT
164 <213> ORGANISM: Salmonella typhimurium
165 <400> SEQUENCE: 8
166      Met Lys Tyr Thr Ile Leu Ser Leu Val Ala Gly Ala Leu Ile Ser Cys
167          1          5          10          15
168      Glu Asn Thr Leu Thr Ser Ala Met Ala Val Lys Met Asn Asp Ala Leu
169          20          25          30
170      Ser Ser Gly Thr Gly Glu Asn Ile Gly Glu Ile Thr Val Ser Glu Thr
171          35          40          45
172      Pro Tyr Gly Leu Leu Phe Thr Pro His Leu Asn Gly Leu Thr Pro Gly
173          50          55          60
174      Ile His Gly Phe His Val His Thr Asn Pro Ser Cys Met Pro Gly Met
175      65          70          75          80
176      Lys Asn Ala Asp Gly Thr Ala Thr Tyr Pro Leu Leu Ala Pro Arg Leu
177          85          90          95
178      Lys Asp Gly Lys Glu Val Pro Ala Leu Met Ala Gly Gly His Leu Asp
179          100          105          110
180      Pro Glu Lys Thr Gly Ser Leu Ser Glu Leu Lys Gly His Ser Leu Met
181          115          120          125
182      Ile His Lys Gly Gly Asp Asn Tyr Ser Lys His Leu Gly Pro Tyr Asn
183          130          135          140
184      Asp Lys Gly His Leu Gly Asp Leu Pro Gly Leu Val Val Asp Lys Pro
185      145          150          155          160
186      Ala Pro Leu Gly Gly Gly Gly Ala Arg Phe Ala Cys Gly Val Ile Glu
187          165          170          175
188      Lys
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 173
192 <212> TYPE: PRT
193 <213> ORGANISM: Photobacterium leignathi
194 <400> SEQUENCE: 9
195      Met Asn Lys Ala Lys Thr Leu Leu Phe Thr Ala Leu Ala Phe Gly Leu
196          1          5          10          15
197      Gln Asp Leu Thr Ser His Gln Ala Leu Ala Val Lys Met Thr Asp Leu
198          20          25          30
199      Gln Thr Gly Lys Pro Val Gly Thr Ile Glu Leu Ser Gln Asn Lys Tyr

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200          35          40          45
201 Gly Val Val Phe Thr Pro Glu Leu Ala Asp Leu Thr Pro Gly Met His
202          50          55          60
203 Gly Phe His Ile His Gln Asn Gly Ser Cys Ala Ser Ser Glu Lys Ser
204          65          70          75          80
205 Ala Asn Gly Leu Ala Thr Asn Pro Val Leu Ala Pro Arg Leu Thr Asp
206          85          90          95
207 Gly Lys Val Val Leu Gly Gly Ala Ala Gly Gly His Tyr Asp Pro Glu
208          100          105          110
209 His Thr Asn Leu Lys Glu Leu Lys Gly His Ala Ile Met Ile His Ala
210          115          120          125
211 Gly Gly Asp Asn His Ser Lys His Gly Phe Pro Trp Thr Asp Asp Asn
212          130          135          140
213 His Lys Gly Asp Leu Pro Ala Leu Phe Val Asp Met Pro Lys Ala Leu
214          145          150          155          160
215 Gly Gly Gly Gly Ala Arg Val Ala Cys Gly Val Ile Gln
216          165          170
218 <210> SEQ ID NO: 10
219 <211> LENGTH: 185
220 <212> TYPE: PRT
221 <213> ORGANISM: Haemophilus parainfluenzae
222 <400> SEQUENCE: 10
223 Met Met Lys Thr Leu Leu Ala Leu Ala Ile Ser Gly Ile Cys His Asp
224      1          5          10          15
225 His Met Ala Lys Pro Ala Gly Pro Ser Ile Glu Ala Ala Gly Val Ala
226          20          25          30
227 Asn Ala Val Lys Val Gln Gln Leu Asp Pro Ala Asn Gly Asn Lys Asp
228          35          40          45
229 Val Gly Thr Val Thr Ile Thr Glu Ser Asn Tyr Gly Leu Val Phe Thr
230          50          55          60
231 Pro Asn Leu Gln Gly Leu Ala Glu Gly Leu His Gly Phe His Ile His
232          65          70          75          80
233 Glu Asn Pro Ser Cys Asp Pro Lys Glu Lys Leu His Asp Gly Thr Ala
234          85          90          95
235 Thr Asn Pro Val Leu Ala Arg Arg Leu Lys Asp Gly Lys Leu Thr Ser
236          100          105          110
237 Gly Leu Ala Ala Gly Gly His Trp Asp Pro Lys Gly Ala Lys Lys Leu
238          115          120          125
239 Asp Glu Val Arg Gly His Ser Ile Met Ile His Ala Gly Gly Asp Asn
240          130          135          140
241 His Ser Gln His Gly Tyr Pro Trp Gln Asp Asp Ala His Leu Gly Asp
242          145          150          155          160
243 Leu Pro Ala Leu Thr Val Asp His Pro Ala Pro Leu Gly Gly Gly Gly
244          165          170          175
245 Pro Arg Met Ala Cys Gly Val Ile Lys
246          180          185
248 <210> SEQ ID NO: 11
249 <211> LENGTH: 173
250 <212> TYPE: PRT

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VERIFICATION SUMMARY

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